FIGURE 1

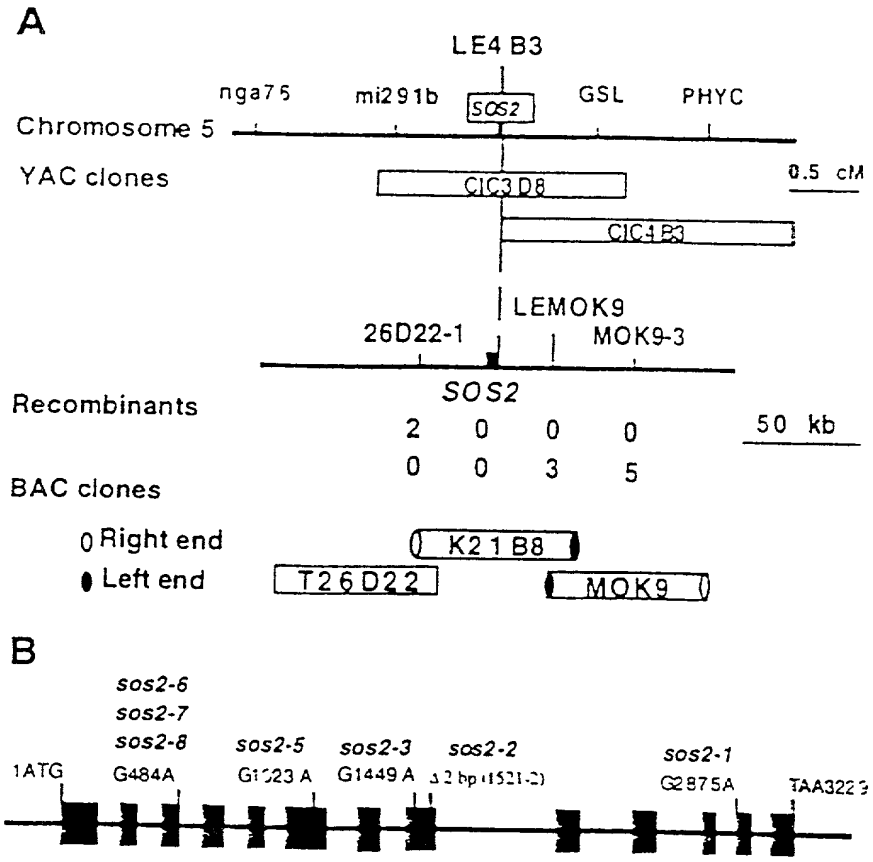

A
LE4 B3
nga76
mi291b
SOS2
GSL
PHYC
Chromosome 5
YAC clones
CIC3D8
0.5 cM
CIC1B3
LEMOK9
26D22-1
MOK9-3
SOS2
Recombinants
2 0 0 0
0 0 3 5
50 kb
BAC clones
0 Right end
Left end
K21B8
T26D22
MOK9
B
sos2-6
sos2-7
sos2-8
G484A
sos2-5
G1023A
sos2-3
G1449A
sos2-2
Δ2 bp (1521-2)
sos2-1
G2875A
1ATG
TAA3223

Figure 2

A


Kinase
Regulatory Domain

B

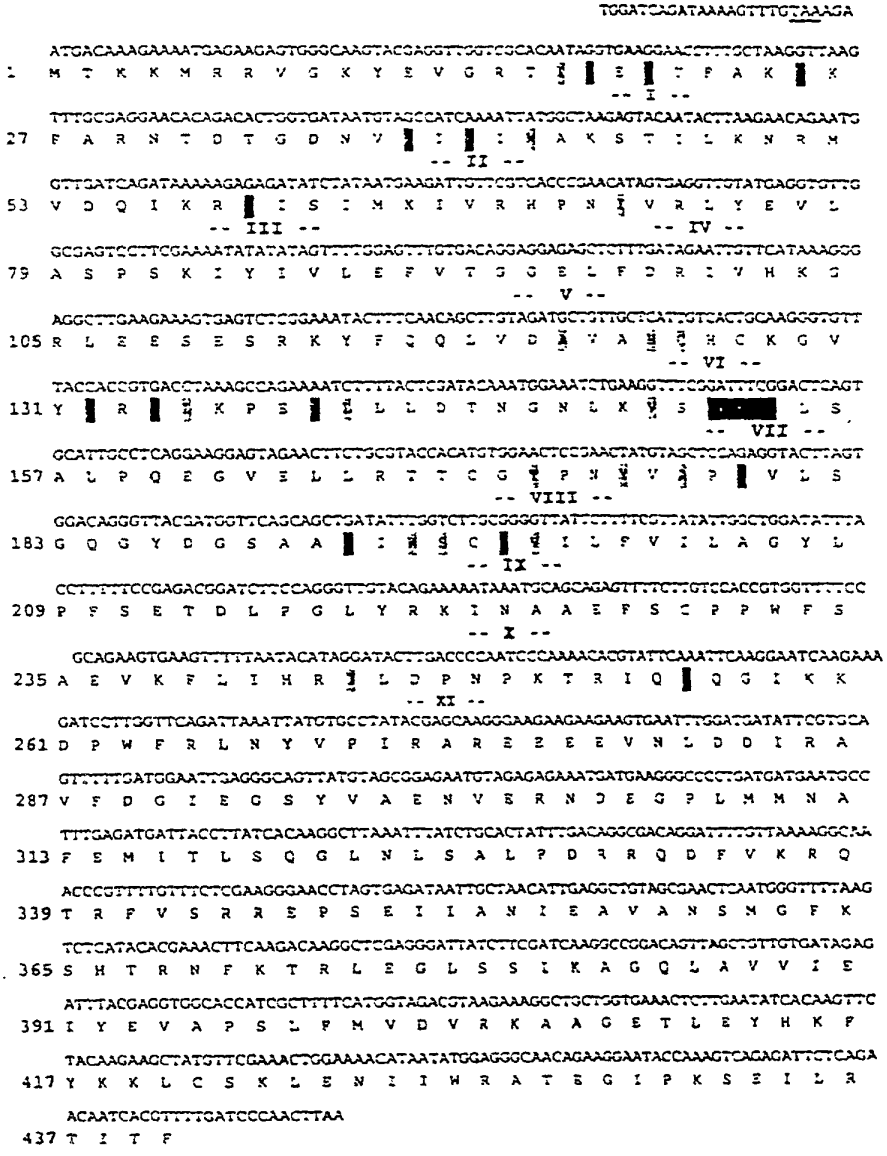

TGGATCAGATAAAAGTTTGTAAAGA
ATGACAAAGAAAATGAGAAGAGTGGGCAAGTACGAGGTTGGTCGCACAATAGGTGAAGGAACTTTTGCTAAGGTTAAG
1 M T K K M R R V G K Y E V G R T I E T P A K K
-- I --
TTTGCGAGGAACACAGACACTGGTGATAATGTAGCCATCAAAATTATGGCTAAGAGTACAATACTTAAGAACAGAATG
27 F A R N T D T G D N V I I K A K S T I L K N R M
-- II --
GTTGATCAGATAAAAAGAGAGATATCTATAATGAAGATTGTTCGTCACCCGAACATAGTGAGGTTGTATGAGGTGTTG
53 V D Q I K R I S I M K I V R H P N I V R L Y E V L
-- III -- -- IV --
GCGAGTCGTTCGAAAATATATATAGTTTTGGAGTTTGTGACAGGAGGAGAGCTCTTTGATAGAATTGTTCATAAAGGG
79 A S P S K I Y I V L E F V T G G E L F D R I V H K G
-- V --
AGGCTTGAAGAAAGTGAGTCTCGGAAATACTTTCAACAGCTTGTAGATGCTGTTGCTCATTGTCACTGCAAGGGTGTT
105 R L E E S E S R K Y F Q Q L V D A V A H C H C K G V
-- VI --
TACCACCGTGACCTAAAGCCAGAAAATCTTTTACTCGATACAAATGGAAATCTGAAGGTTTCGGATTTCGGACTCAGT
131 Y H R D K P E N L L D T N G N L K V S D F G L S
-- VII --
GCATTGCCTCAGGAAGGAGTAGAACTTCTGCGTACCACATGTGGAACTCCGAACTATGTAGCTCCAGAGGTACTTAGT
157 A L P Q E G V E L L R T T C G T P N Y V A P E V L S
-- VIII --
GGACAGGGTTACGATGGTTCAGCAGCTGATATTTGGTCTTGCGGGGTTATTCTTTTCGTTATATTGGCTGGATATTTA
183 G Q G Y D G S A A D I W S C I L F V L A G Y L
-- IX --
CCTTTTTCCGAGACGGATCTTCCAGGGTTGTACAGAAAAATAAATGCAGCAGATTTTCTTGTCCACCGTGGTTTTCC
209 P F S E T D L P G L Y R K I N A A E F S C P P W F S
-- X --
GCAGAAGTGAAGTTTTTAATACATAGGATACTTGACCCCAATCCCAAAACACGTATTCAAATTCAAGGAATCAAGAAA
235 A E V K F L I H R D L D P N P K T R I Q D Q G I K K
-- XI --
GATCCTTGGTTCAGATTAAATTATGTGCCTATACGAGCAAGGGAAGAAGAAGAAGTGAATTTGGATGATATTCGTGCA
261 D P W F R L N Y V P I R A R E E E E V N L D D I R A
GTTTTTGATGGAATTGAGGGCAGTTATGTAGCGGAGAATGTAGAGAGAAATGATGAAGGGCCCCTGATGATGAATGCC
287 V F D G I E G S Y V A E N V E R N D E G P L M M N A
TTTGAGATGATTACCTTATCACAAGGCTTAAAATTTATCTGCACTATTTGACAGGCGACAGGATTTTGTTAAAAGGCAA
313 F E M I T L S Q G L N L S A L P D R R Q D F V K R Q
ACCCGTTTTGTTTCTCGAAGGGAACCTAGTGAGATAATTGCTAACATTGAGGCTGTAGCGAACTCAATGGGTTTTAAG
339 T R F V S R R E P S E I I A N I E A V A N S M G F K
TCTCATACACGAAACTTCAAGACAAGGCTCGAGGGATTATCTTCGATCAAGGCCGGACAGTTAGCTGTTGTGATAGAG
365 S H T R N F K T R L E G L S S I K A G Q L A V V I E
ATTTACGAGGTGGCACCATCGCTTTTCATGGTAGACGTAAGAAAGGCTGCTGGTGAAACTCTTGAATATCACAAGTTC
391 I Y E V A P S L F M V D V R K A A G E T L E Y H K F
TACAAGAAGCTATGTTCGAAACTGGAAAACATAATATGGAGGGCAACAGAAGGAATACCAAAGTCAGAGATTCTCAGA
417 Y K K L C S K L E N I I W R A T E G I P K S E I L R
ACAATCACGTTTTGATCCCAACTTAA
437 T I T F

Figure 3

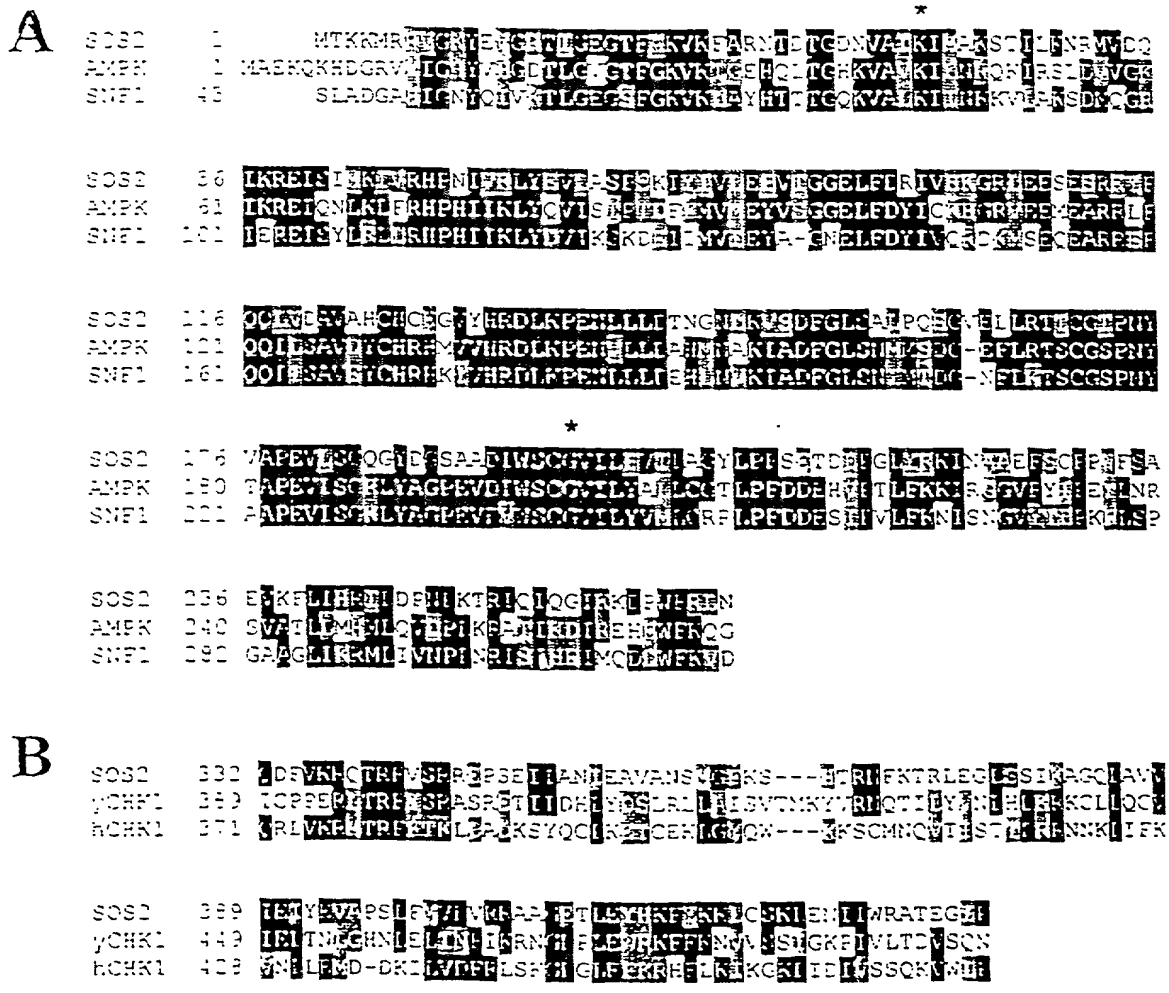


Figure 4

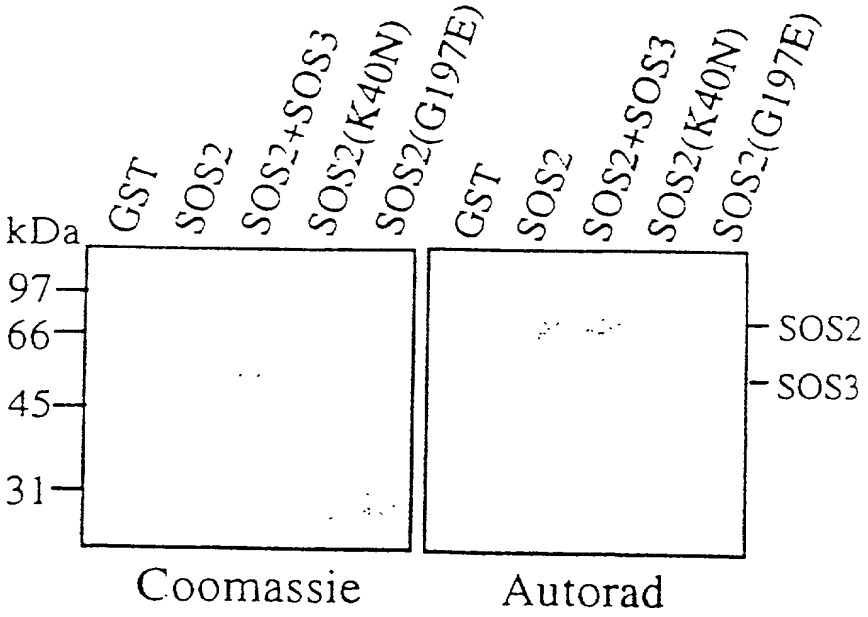
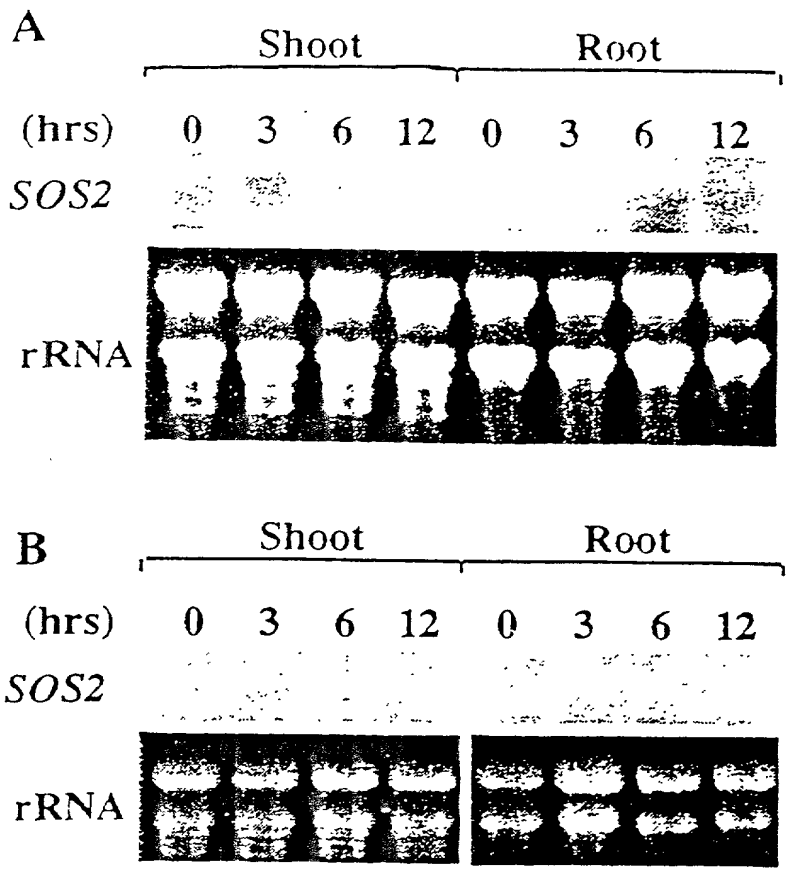

GST
SOS2
SOS2+SOS3
SOS2(K40N)
SOS2(G197E)
GST
SOS2
SOS2+SOS3
SOS2(K40N)
SOS2(G197E)
kDa
97
66
45
31
SOS2
SOS3
Coomassie
Autorad

Figure 5


A
Shoot
Root
(hrs)
0 3 6 12 0 3 6 12
SOS2
rRNA
B
Shoot
Root
(hrs)
0 3 6 12 0 3 6 12
SOS2
rRNA